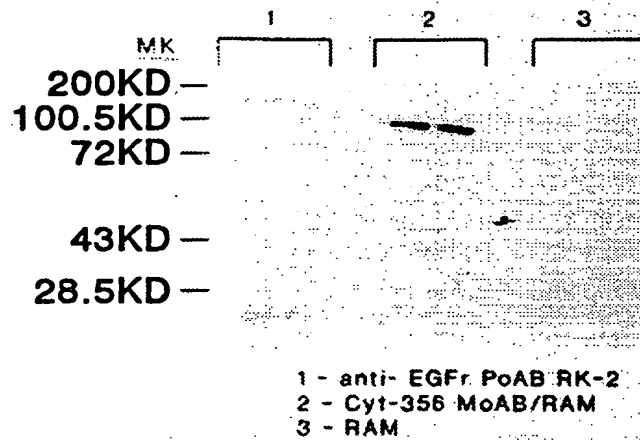


1/48

08/466381

FIGURE 1



08/466381

2/48

FIGURE 2A

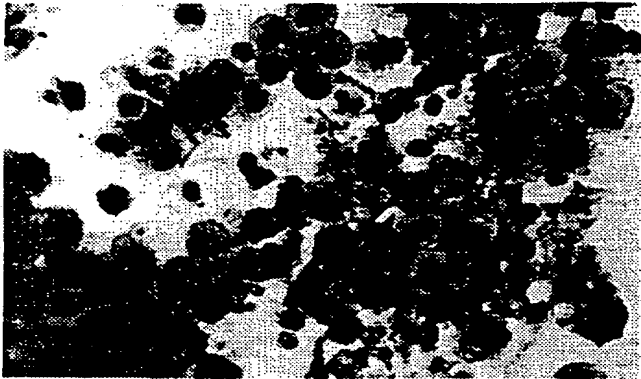


FIGURE 2B

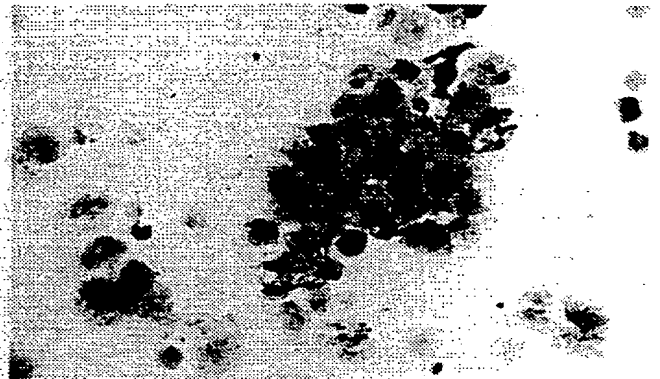
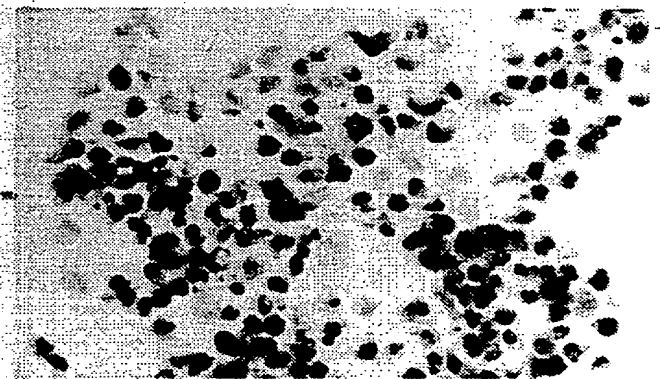


FIGURE 2C



FIGURE 2D



08, '466381

3/48

FIGURE 3A

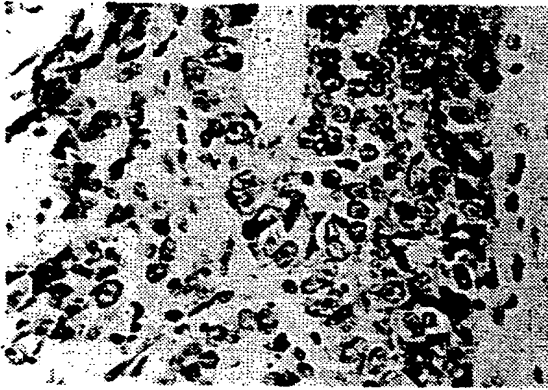


FIGURE 3B

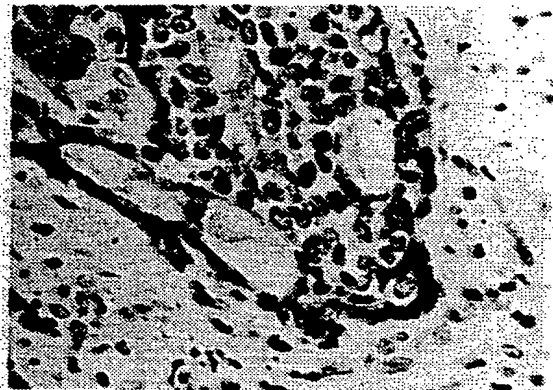


FIGURE 3C

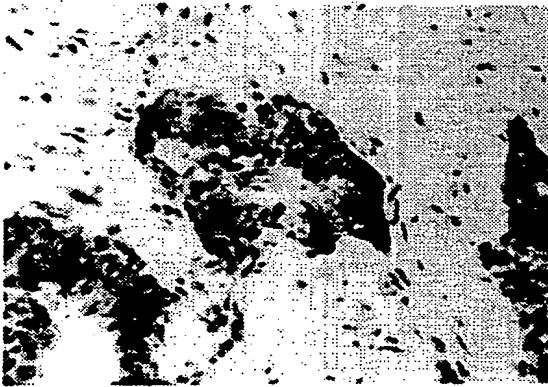
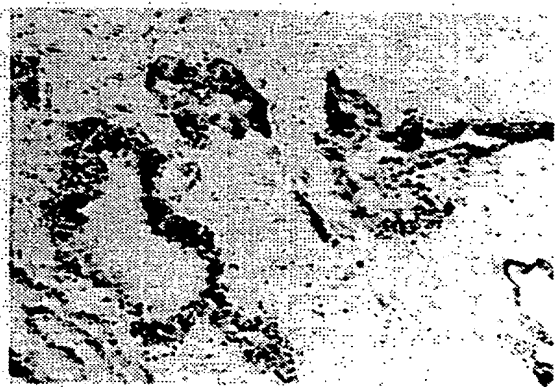


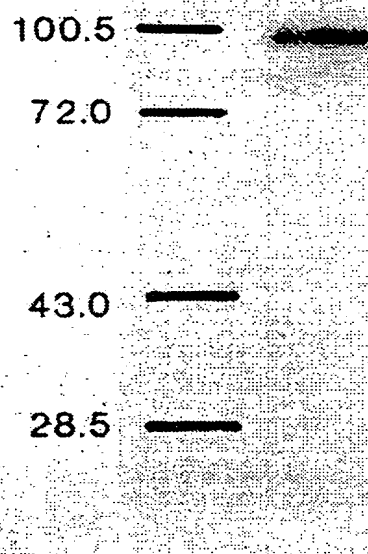
FIGURE 3D



08/466381

4/48

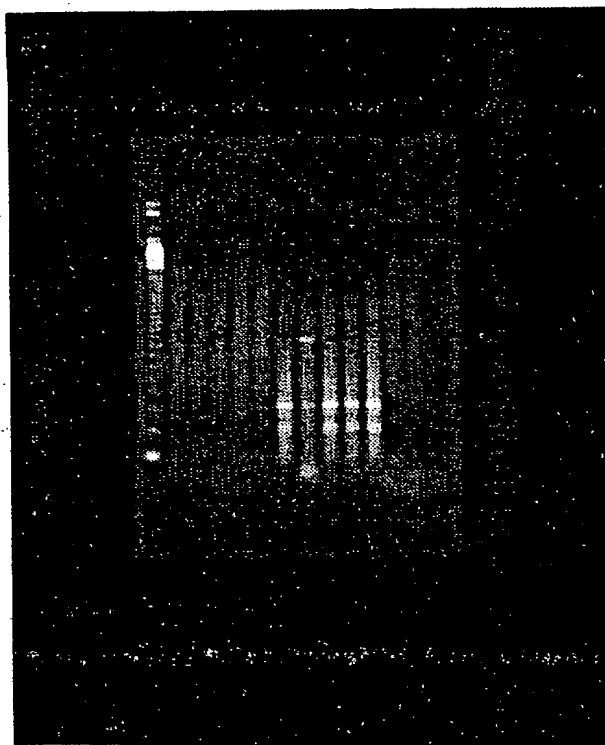
FIGURE 4



08/466381

5/48

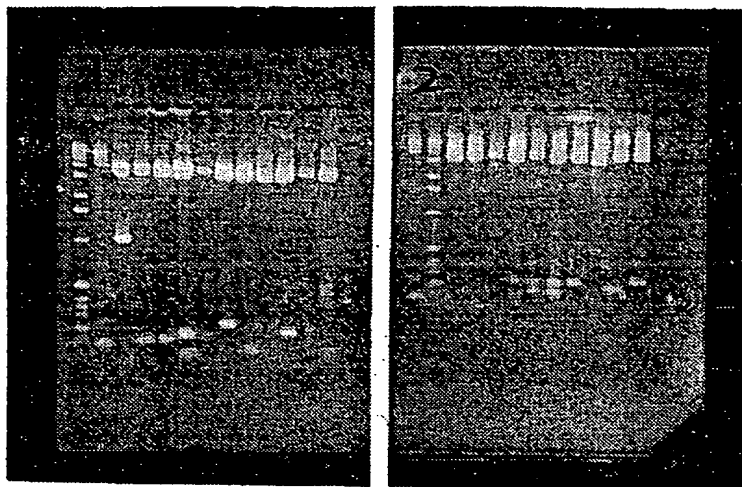
FIGURE 5



08, 466381

6/48

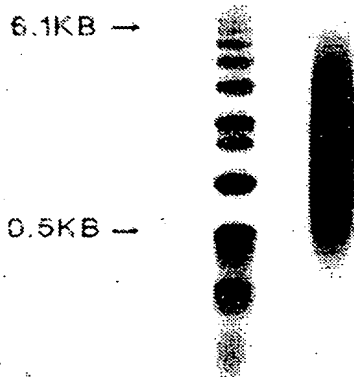
FIGURE 6A FIGURE 6B



08/466381

7/48

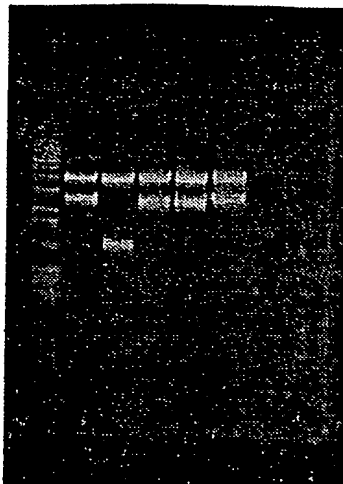
FIGURE 7



8/48

08/466381

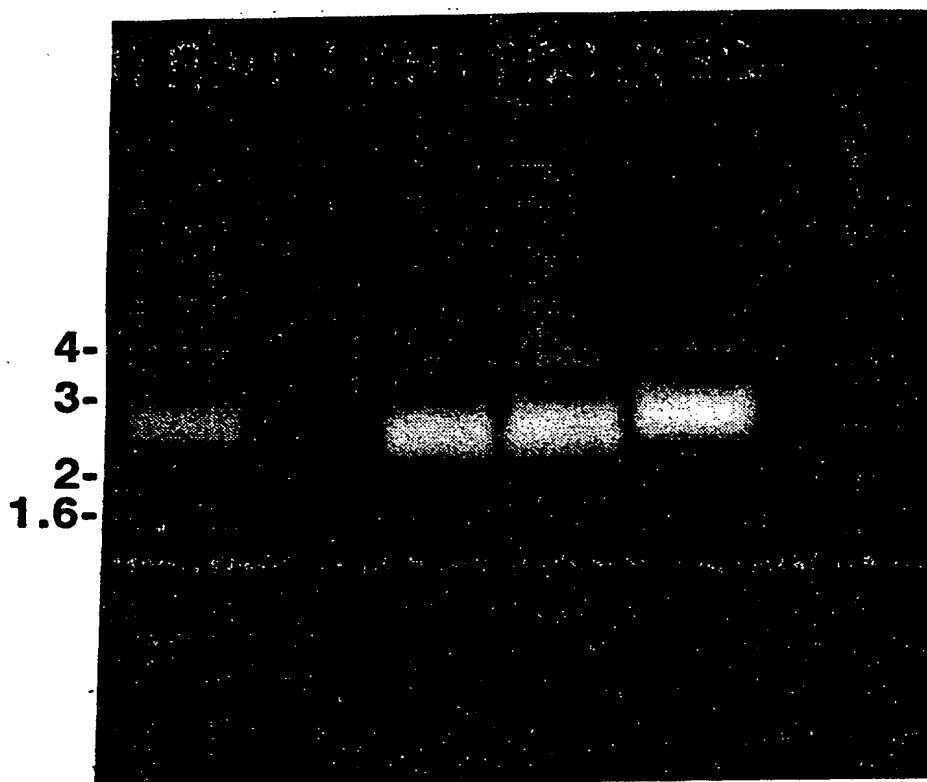
FIGURE 8



08/466381

9/48

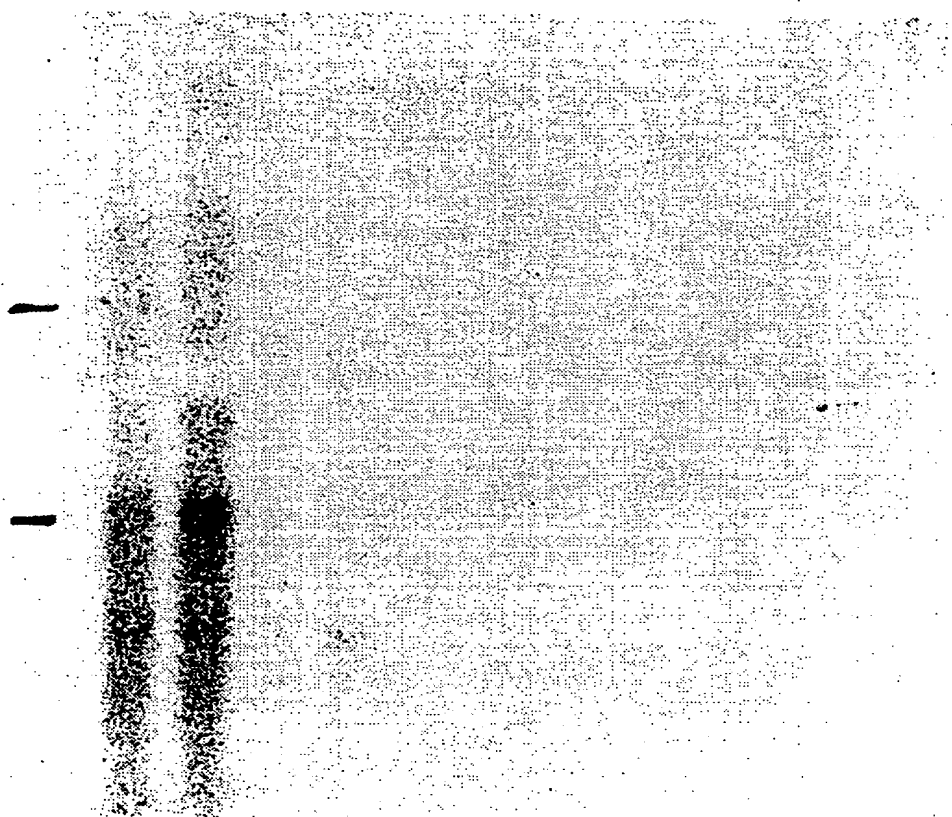
FIGURE 9



08/466381

10/48

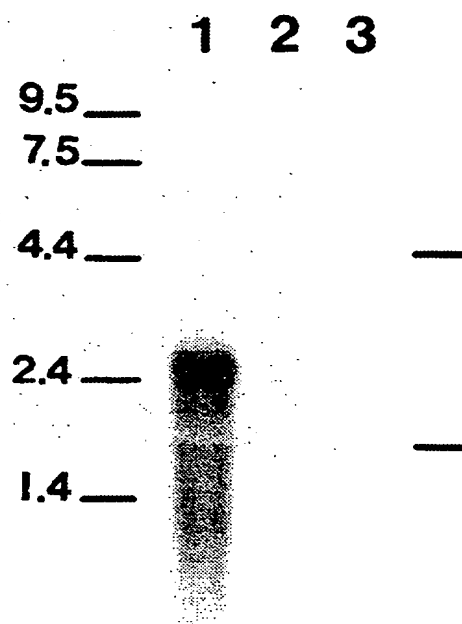
FIGURE 10



08/466381

11/48

FIGURE 11



08/466381

12/48

FIGURE 12A

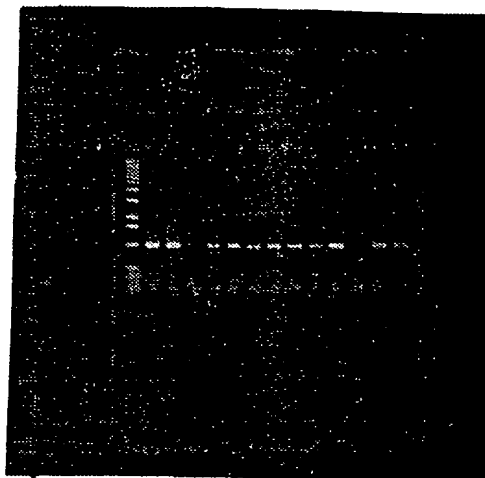
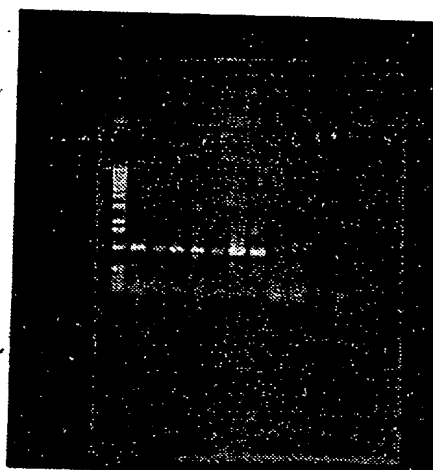


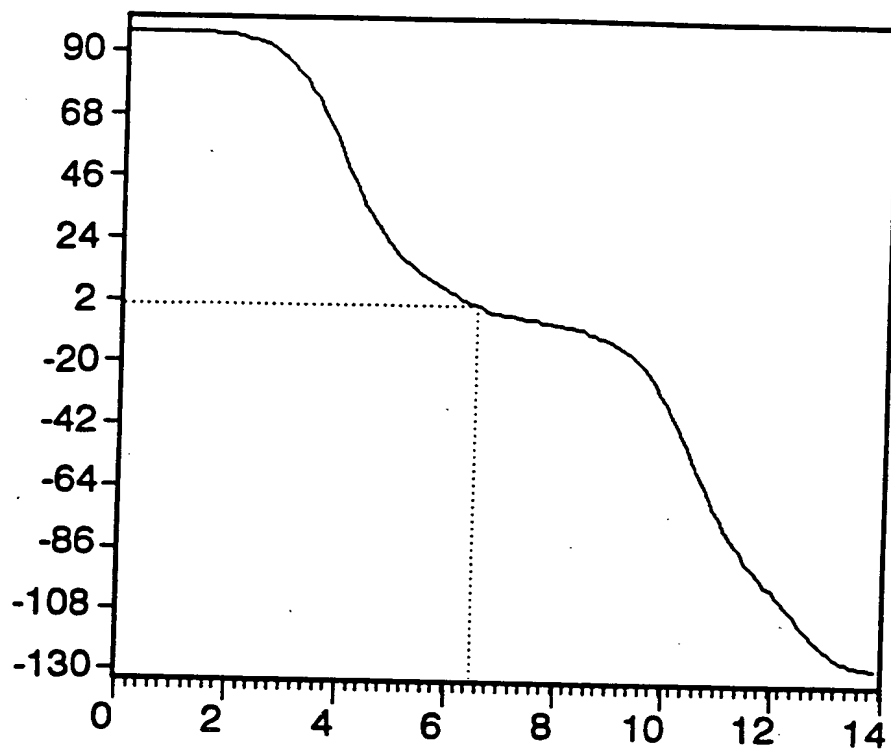
FIGURE 12B



08/466381

13/48

FIGURE 13



16/48

FIGURE 14-3

451 E E C S E E T T E E E E E E E E E E H H H H H H H H H H
481 H C S H H H H H H H H H H T T T C C C T E E E E E E
511 E E E E E C C C E E E E H H H H H H T C C C E E T E C T
541 T E T T T C E E E E E E E E E E H H H H H H H H H H
571 H H H H H E E E E E E E E E E H H H H H H T H H H
601 H E E E E E
631 H H H H H H H H H H H H H H H H H H T T C C E E E E
661 E E H H H H H H H H H H H H E E T T C C C T E E E E E E
691 E E E T C C C C T E E E E E E E E H H H H H H H C C
721 C H

17/48

08/466381

FIGURE 14-4

Semi-graphical output.

=====

Symbols used in the semi-graphical representation:

Helical conformation: X	Extended conformation: -
Turn conformation: >	Coil conformation: *

10	20	30	40	50
MWNL	HTDS	AVATARR	PRWLCAGALV	LAGGFFLLGFLFGWFIKSSNEAT

XXXXXXXXXXXXX	----	XXXXXXXXXXXXX
>	>	>
XXXXXXXXXXXXX	----	XXXXXXXXXXXXX
>	>	>

60	70	80	90	100
NITPKHNMKAFL	DELKAENIKKFLYNFTQI	PHLAGTEQN	FQLAKQIQSQW	

08/466381

18/48

FIGURE 14-5

```

XXXXXXXXXXXXXXXXXXXX-->>-----XXXXXXXXXXXXX-X*--
XXXXXXXXXXXXXXXXXXXX-->>-----XXXXXXXXXXXXX-X*--

110      120      130      140      150
|         |         |         |         |
KEFGDSVELAHYDVLLSYPNKTHPNYISINEDGNEIFNTSLFEPPPG

->>>*****-->>>----->>>*****>
->>>*****-->>>----->>>*****>

160      170      180      190      200
|         |         |         |         |
YENVSDIVPPFSAFSPQGMPEGDLVVVNYARTEDFFKLERDMKINCSGKI

```


08/466381

20/48

FIGURE 14-7

410 | 420 430 440 450
SFGTLKKEGWRPRRTILFASWDAAEEFGLGSTWEAENSRLQERGVAI

```
--XXXXXXXXXX*XXXXXXXXX<*^>*>XXXXX
--XXXXXXXXXX*XXXXXXXXX<*^>*>XXXXX
```

460 470 480 490 500
NADSSIEGNYTLRVDC TPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKK

><XXXXXXXXXX><XXXXXXXXXX*><XXXXXXXXXX
 ><XXXXXXXXXX><XXXXXXXXXX*><XXXXXXXXXX

510 520 530 540 550
SPSPFSGMPRIKLGSGNDFEVFFQRLGIASGRARYTKNWTNKFSGYP

Two vertical dashed lines. Each line has an arrow pointing up at the top and an arrow pointing down at the bottom. Between the arrows, there is a central block of 'X's. The left line has 10 'X's, and the right line has 10 'X's. The 'X's are arranged in a grid-like pattern, with 5 rows of 2 'X's each. The lines are separated by a small gap.

A vertical scale with tick marks at 560, 570, 580, 590, and 600.

08/466381

21/48

FIGURE 14-8

LYHSVYETVELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY

-----XXXXXXXXXXXXX-X-----XXXXX----->XXX
 -----XXXXXXXXXXXXX-X-----XXXXX----->XXX

610 620 630 640 650
 | | | | |
 AVVLRKYADKIYISMKHPQEMKTYSVSFDLSFAVKNFTEIASKFSERL

XXXXXXXXXX-----X*XXXXX-----XXXXXXXXXXXXXXXXXXXX
 XXXXXXXXXXXX-----X*XXXXX-----XXXXXXXXXXXXXXXXXXXX

660 670 680 690 700
 | | | | |
 QDFDKSNPIVLRMMNDQLMCLERAFIDPLGLPDRPFYRHVIYAPSSHNKY

XX>>>*>-----XXXXXXXXXX-->>***>----->***>
 XX>>>*>-----XXXXXXXXXX-->>***>----->***>

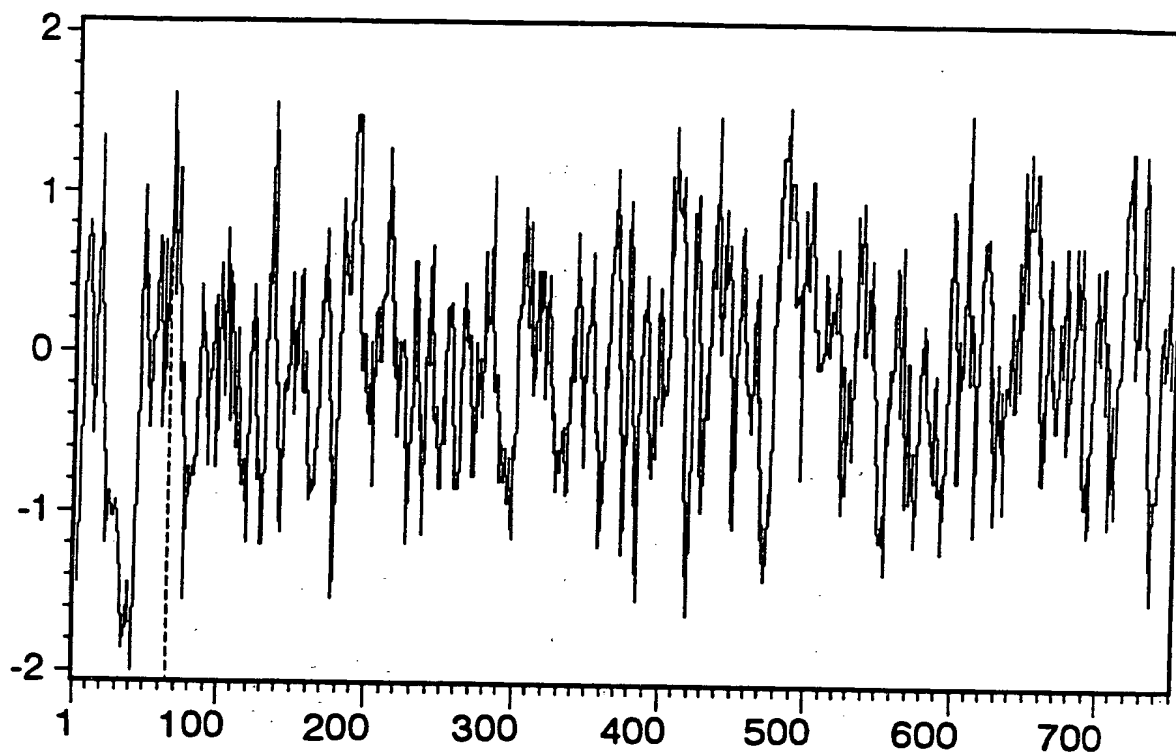
710 720 730 740 750
 | | | | |
 AGESFPGIYDALFDIESKVDPSKANGEVKRQIYVAAFTVQAAETLSEVA

----->-----XXXXXXXXXX**XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX
 ----->-----XXXXXXXXXX**XXXXXXXXXX-----XXXXXXXXXXXXXXXXXX

08/466381

22/48

FIGURE 15A



08/466381

23/48

FIGURE 15B

 * PREDICTION OF ANTIGENIC DETERMINANTS *

Done on sequence PMSANTIGEN.

Total number of residues is: 750.

Analysis done on the complete sequence.

The method used is that of Hopp and Woods.

The averaging group length is: 6 amino acids.

-> This is the value recommended by the authors <-

The three highest points of hydrophilicity are:

(1)	Ah= 1.62	: From	63 to	68	: Asp-Glu-Leu-Lys-Ala-Glu
(2)	Ah= 1.57	: From	132 to	137	: Asn-Glu-Asp-Gly-Asn-Glu
(3)	Ah= 1.55	: From	482 to	487	: Lys-Ser-Pro-Asp-Glu-Gly

Ah stands for: Average hydrophilicity.

Note that, on a group of control proteins, only the highest point was in 100% of the cases assigned to a known antigenic group. The second and third point gave a proportion of 33% of incorrect predictions.

FIGURE 16-2

```

1200      1210      1220      1230      1240      1250
pmsgen AGCACCA CAGATAGCAGCTGGAGAGGAAGTCTCAAGTGCCCTACAAATGTTGGACCTGG
      : : : : : : : : : : : : : : : : : : : : : :
CHKTFE CACATGCTCTGA-AG--GTTGGAAAGGTGCGGATCCA----TTCCTGTAAGGT--GAC--AA
1170      1180      1190      1200      1210

1260      1270      1280      1290      1300      1310
pmsgen CTTTACTGGAAACTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGT
      : : : : : : : : : : : : : : : : : : : : : :
CHKTFE CAAAGCAGGAGA----GCCAGA-TAATGGTGAAACTAGATGTGAACAATTC CATGAAAGA
1220      1230      1240      1250      1260

1320      1330      1340      1350      1360      1370
pmsgen GACAAGAAATTACAAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACCAACAGACAGATATGT
      : : : : : : : : : : : : : : : : : : : : : :
CHKTFE CAGGAAGATTCTGAACATCTTCGGTGCTATCCAGGGATTGGAAGAACCTGATCCGGTATGT
1270      1280      1290      1300      1310      1320

1380      1390      1400      1410      1420      1430
pmsgen CATCTGGGAGGTACCCGGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAGAGTGGAGC
      : : : : : : : : : : : : : : : : : : : : : :
CHKTFE TGTGATTGGAGCCCAAGAGAGACTCCTGGGGCCCCAGGAGTGGCTAAAGCTGGCACTGGAAC
1330      1340      1350      1360      1370      1380

```


08/466381

27/48

FIGURE 16-4

```

1680      1690      1700      1710      1720      1730
pmsgen TACAGCTTGGTACACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CHKTFE TATATGCTGCTGGGAGTATTATGAAGGGGTGAAGAATCCAGCAGCAGTCTCAGAGAGC
1630      1640      1650      1660      1670      1680

1740      1750      1760      1770      1780      1790
pmsgen AAATCTCTTTATGAAAGTTGGACTAAATAAGTCCTTCCCCAGAGTTCAGTGGCATGCC
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
CHKTFE -----CTCTATAACAGACTTGGCCCCAGACTGGGTAAAGCAGTTGTTCCCTCTTGGCCTGGA
1690      1700      1710      1720      1730

```


08/466381

FIGURE 16-9

Accession	Human transferrin receptor mRNA, complete cd	145	145	266
HUMTFRR	54.3% identity in 464 nt overlap			

	1230	1240	1250	1260	1270
pmsgen	AGGAAGTCTCAAAGTGCCCTACAATGTGGACCTGGCTTAC-TGGAAACTTTCTACAC				
			:	:	:
			:	:	:
HUMTFR	TATGGAAGGAGACTGTCCCTCTGACTGGAAAACAGACTCTACATGTAGGATGGTAACCTC				
	1140	1150	1160	1170	1180
					1190

```

1280      1290      1300      1310      1320      1330
pmsgen AAAAGTCAAGATGCACATC-CACTCT-ACCAATG-----AAGTGACAAGAAATTACAA
      : : : : : : : : : : : : : : : : : : : : : :
HUNTER AGAAAGCAAGAAATGTGAAGCTCACTGTGAGCAATGTGCTGAAAGAGATAAAAATTCTTAA
1200      1210      1220      1230      1240      1250

```

pmggen TGTGATAGGTA**CTCTCAGAGGACGAGTGGAACCAGACAGATATGTCATTCTGGAGGTCA**

HUNTFR CATCTTGGAGTTATTAAGGCTTTGTAGAACCAGATCACTATGTTGTAGTTGGGCCCA

	1400	1410	1420	1430	1440	1450
pmsgen	CCGGACTCATGGGTGTTGGTGTATTGACCTCAGAGT-GGAGCAGCTGTTGTTTCATG					
	: :	: : : : : :	: :	: : : : : :	: : : : : :	: :
HUMTFR	GAGAGATGCATGGGGCCCTGGAGCTGCAAAATC-CGGTGTAGGCACAGCTCTCCTATTGA					
	1320	1330	1340	1350	1360	1370

34/48

08/466381

FIGURE 16-11

1690	1700	1710	1720	1730	1740
pmsgen	ACAACCTAACAAAGAGCTGAAAGCCCTGATGAAGGCTTTGAAGGCAAAATCTCTTATG				
:	:	:	:	:	:
:	:	:	:	:	:
HUMTFR	AAAACAATGC AAAATGTGAAGCATCCGGTACTGGGCAATTTCTATATCAGGACAGCAAC				
1620	1630	1640	1650	1660	1670

08/466381

35/48

FIGURE 17A

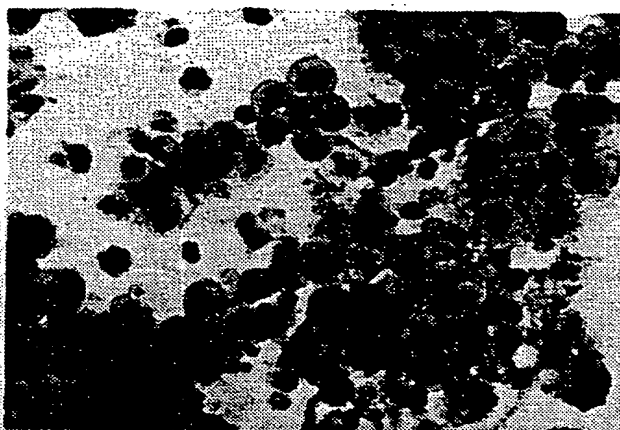


FIGURE 17B

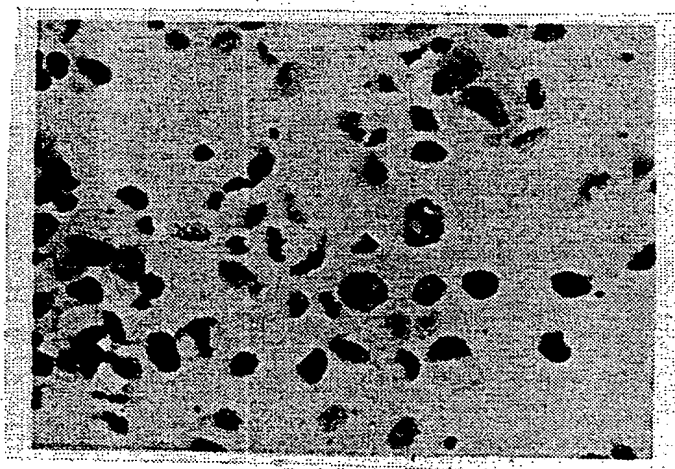
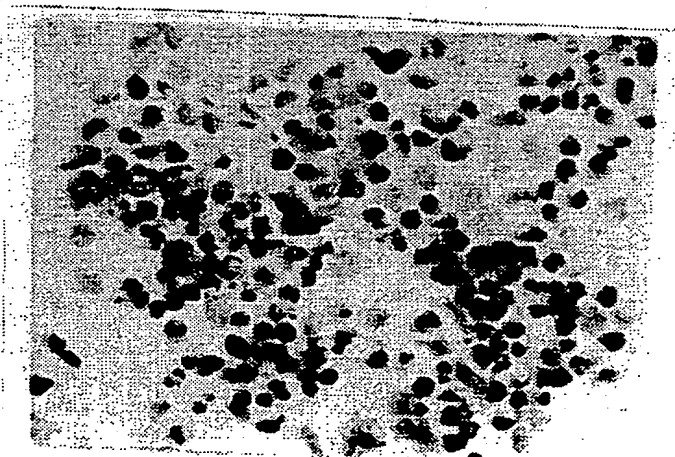


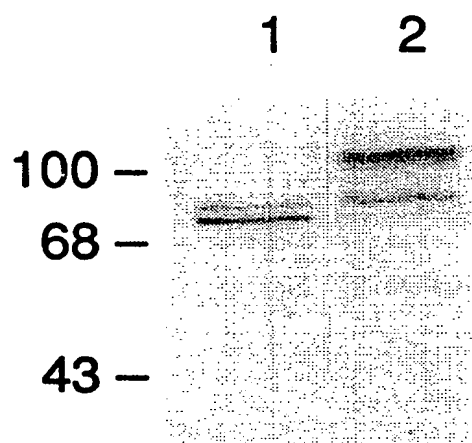
FIGURE 17C



08/466381

36/48

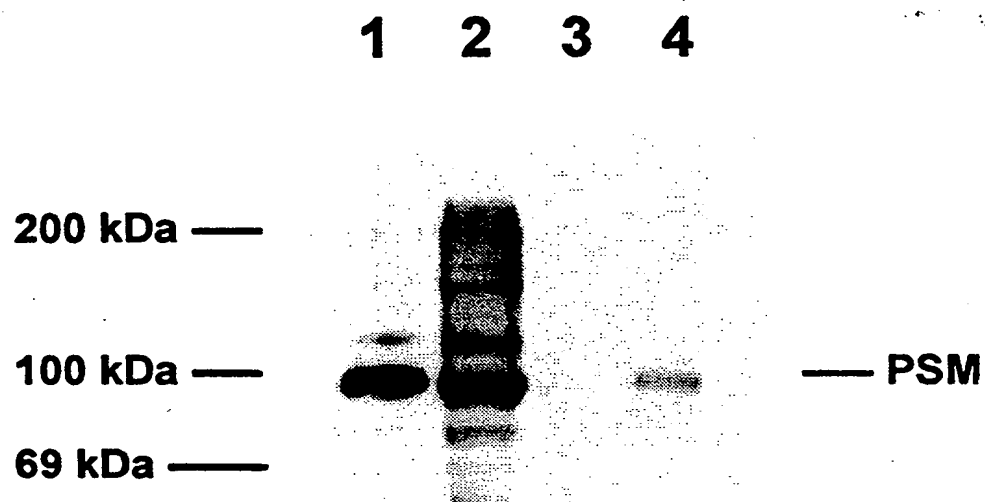
FIGURE 18



08/466381

37/48

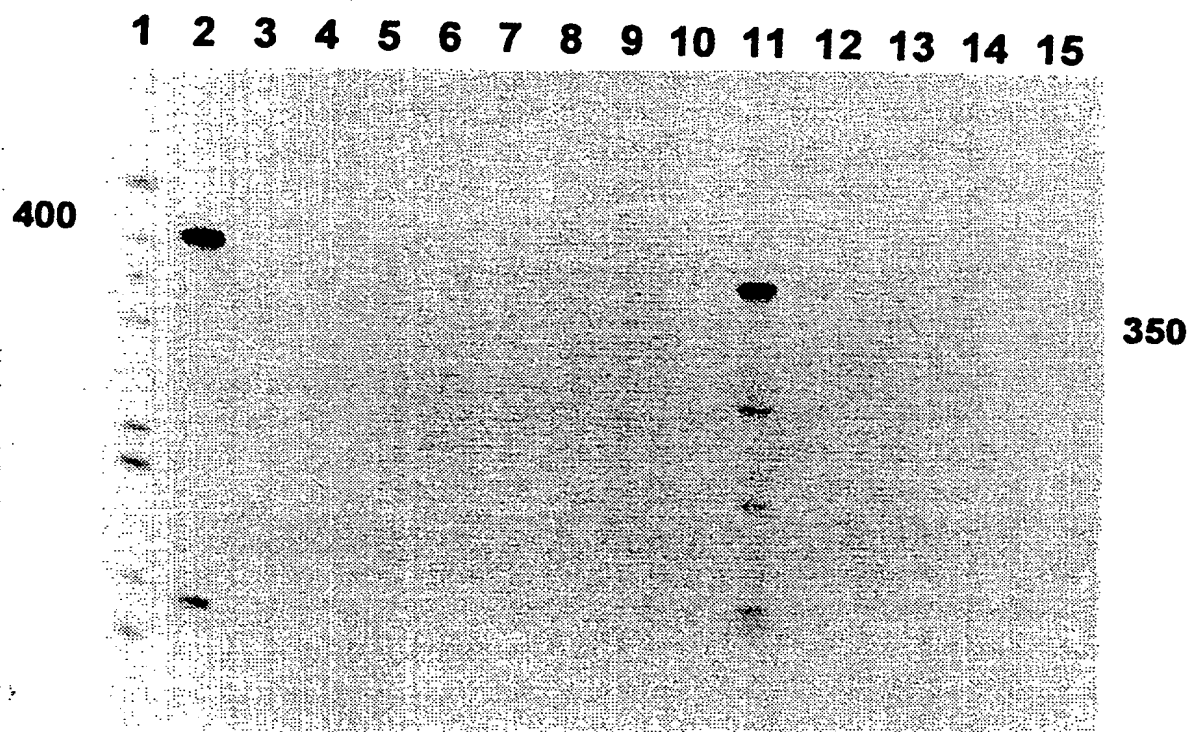
FIGURE 19



08/466381

38/48

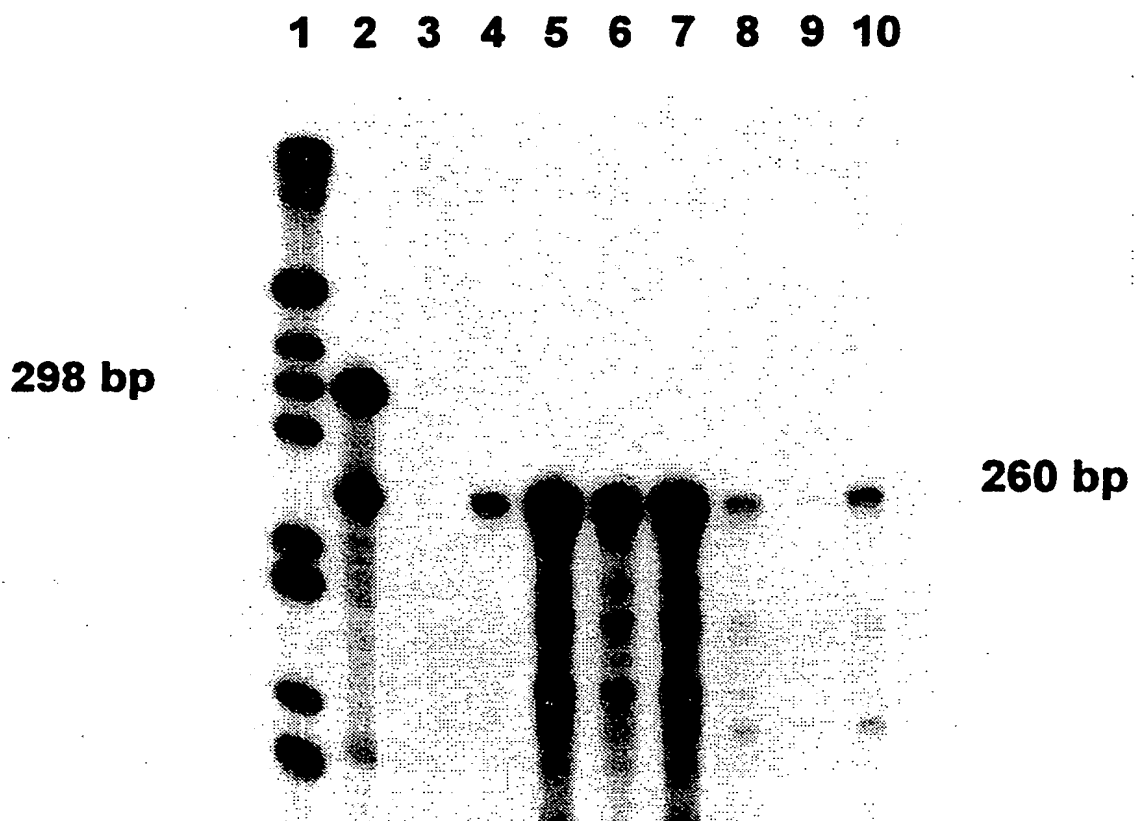
FIGURE 20



08/466381

39/48

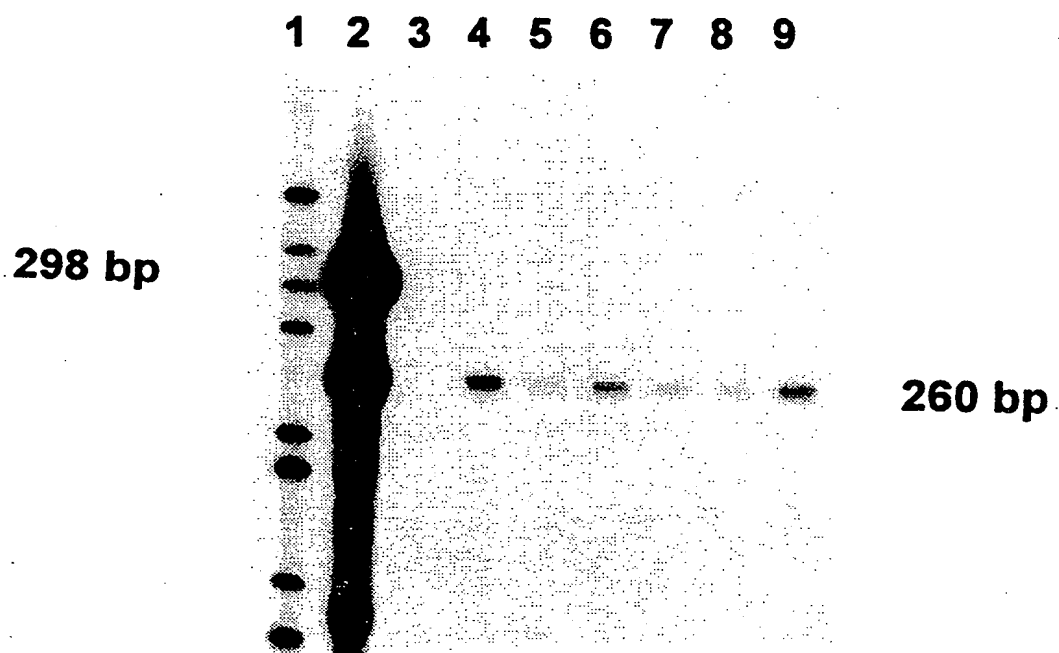
FIGURE 21



08/466381

40/48

FIGURE 22



08/466381

41/48
FIGURE 23

CELL LINE/TYPE	11p11.2-13 REGION	METASTATIC	PSM RNA DETECTED	PSM DNA DETECTED
LNCap			++	ND
HUMAN PROSTATE			++	ND
A9 (FIBROSARCOMA)	NO	NO	-	-
A9(11) (A9+HUM. 11)	YES	NO	-	REPEAT
AT6.1 (RAT PROSTATE)	NO	YES	-	-
AT6.1-11-c11	YES	NO	+	++
AT6.1-11-c12	NO	YES	-	-
R1564 (RAT MAMMARY)	NO	YES	-	-
R1564-11-c14	YES	YES	-	+
R1564-11-c15	YES	YES	-	REPEAT
R1564-11-c16	YES	YES	-	ND
R1564-11-c12	YES	YES	ND	+

08/466381

42/48

FIGURE 24A

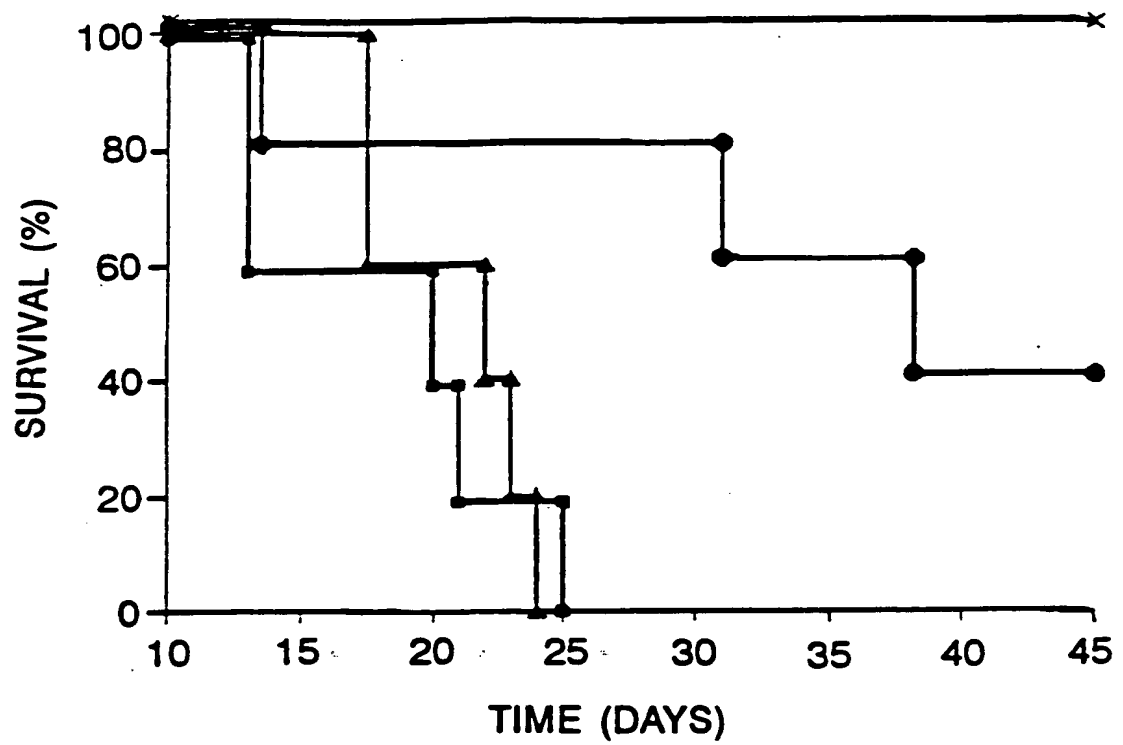
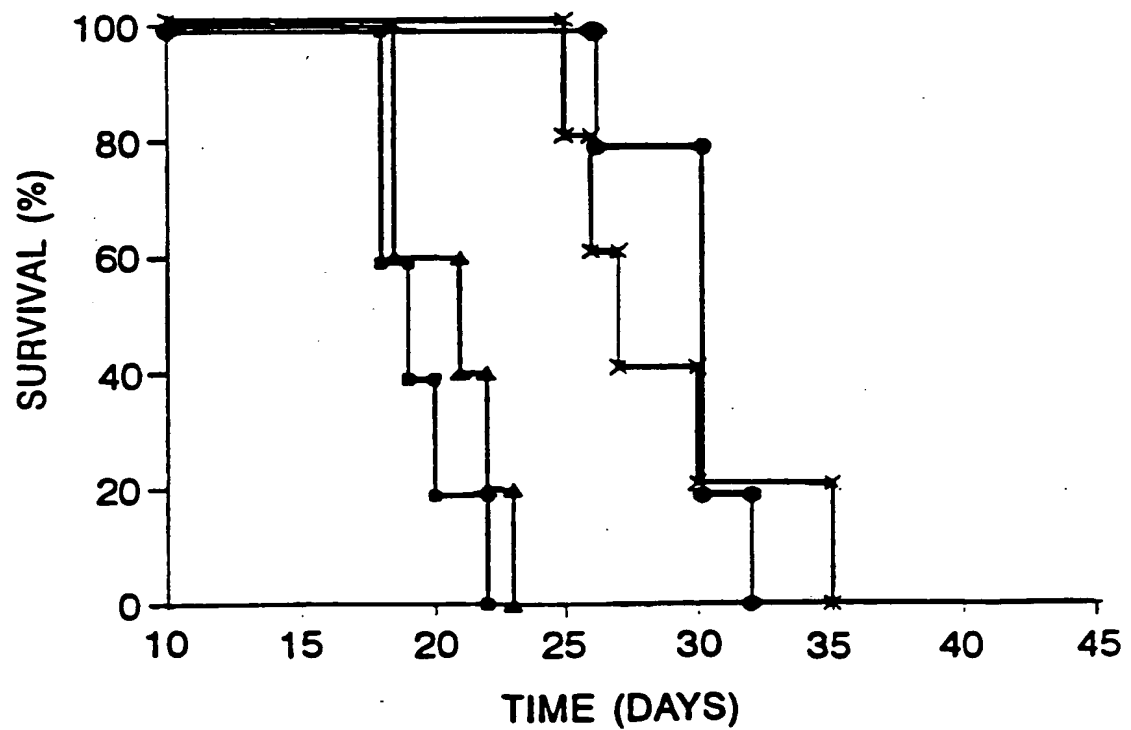


FIGURE 24B



43/48

08/466381

FIGURE 25A

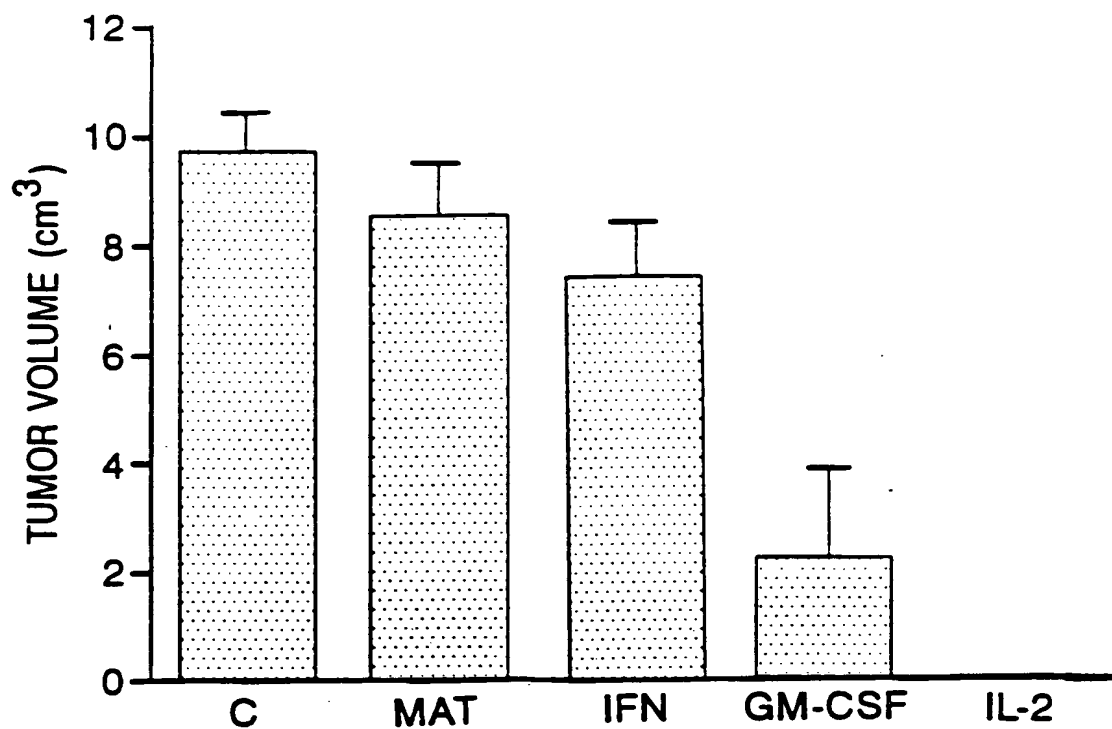
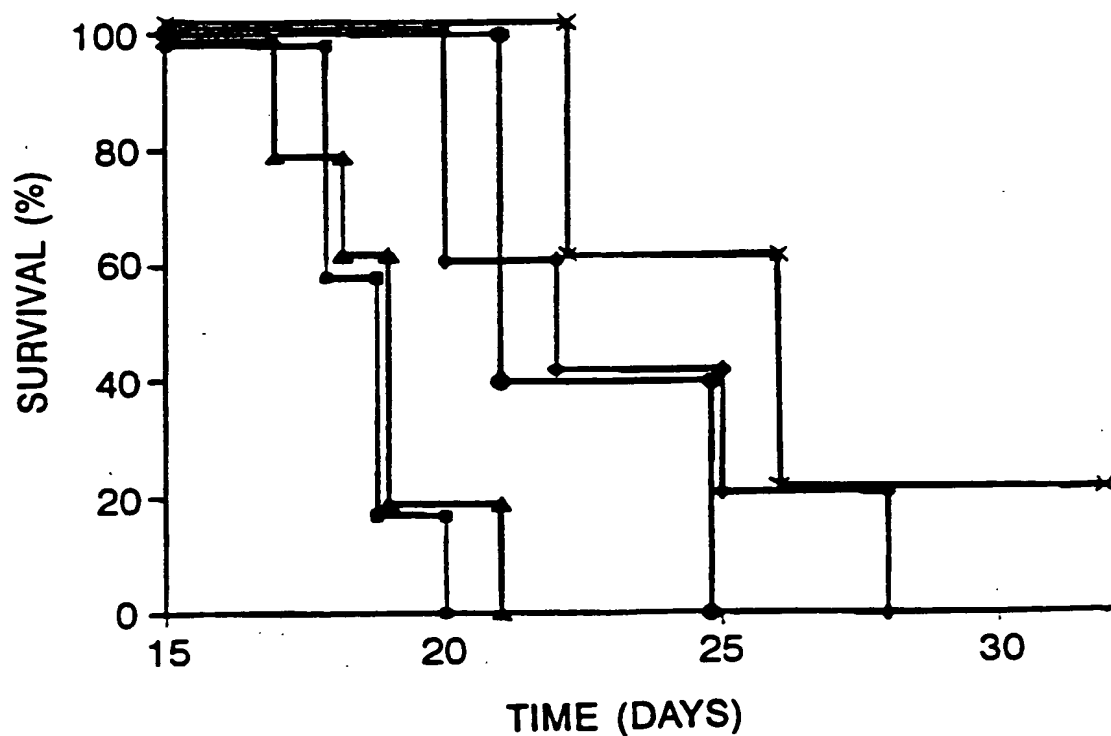


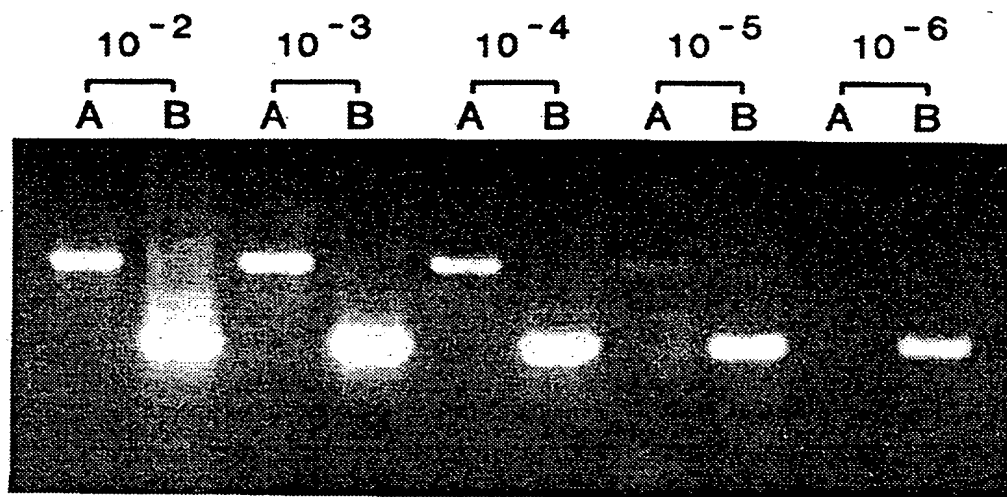
FIGURE 25B



08/466381

44/48

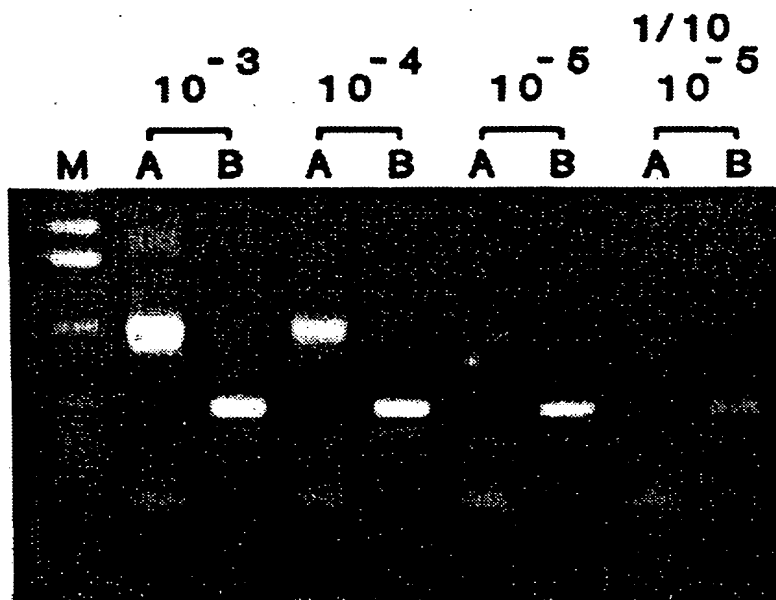
FIGURE 26



08/466381

45/48

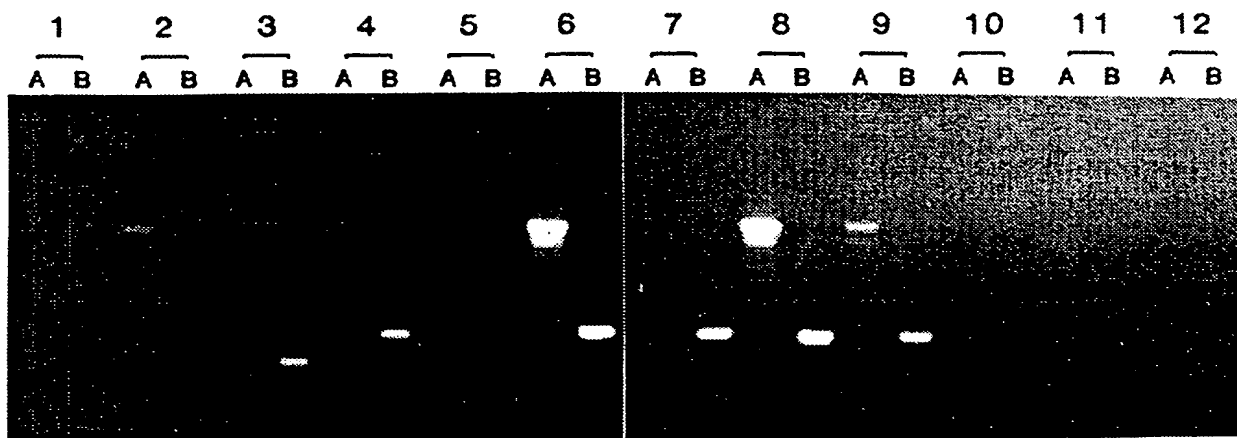
FIGURE 27



08/466381

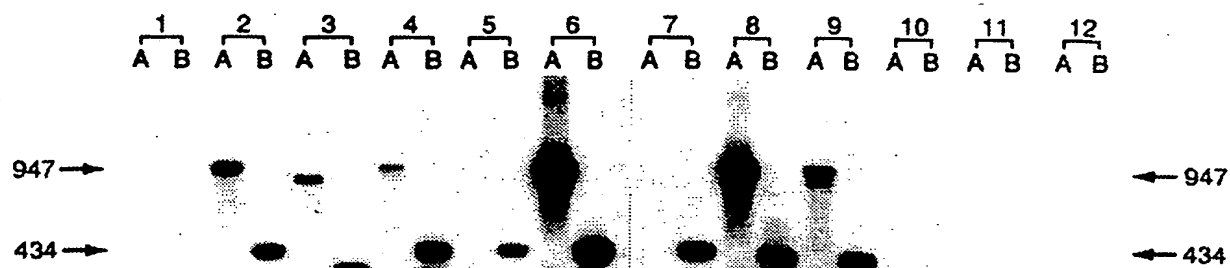
46/48

FIGURE 28



47/48

FIGURE 29



08/466381

48/48
FIGURE 30

Patient	Stage	Treatment	PSA	PAP	PSA-PCR	PSM-PCR
1	T2NxMo	None	8.9	0.7	-	+
2	T2NoMo	RRP 7/93	6.1	-	-	+
3	T2CNoMo	PLND 5/93	4.5	0.1	-	+
4	T2BNoMo	RRP 3/92	NMA	0.4	-	+
5	T3NxMo	Proscar + Flutamide	51.3	1.0	-	+
6	Recur T3	I-125 1986	54.7	1.4	-	+
7	T3ANoMo	RRP 10/92	NMA	0.3	-	+
8	T3NxMo	XRT 1987	7.5	0.1	-	-
9	T3NxMo	Proscar + Flutamide	35.4	0.7	-	-
10	D2	S/P XRT Flutamide + Emcyt	311	4.5	+	+
11	D2	RRP 4/91 Lupron 10/92 Velban + Emcyt 12/92	1534	1.4	+	+
12	T2NoMo	RRP 8/91	NMA	0.5	-	+
13	T3NoMo	RRP 1/88 Lupron + Flutamide 5/92	0.1	0.3	-	-
14	D1	PLND 1989 XRT 1989	1.6	0.4	-	-
15	D1	Proscar + Flutamide	20.8	0.5	-	-
16	T2CNoMo	RRP 4/92	0.1	0.3	-	-

SUBSTITUTE SHEET (RULE 26)